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(54) Title: **GENETIC ANALYSIS**

(57) Abstract: A method is described for use in whole genome analysis. The method - termed inter-population perfectly matched duplex depletion - can overcome many of the limitations of current approaches based upon SNPs and linkage disequilibrium within isolated populations. Inter-population perfectly matched duplex depletion isolates a fragment (or fragments) containing differences between the "affected" and "unaffected" populations or cells. A convenient method - terminal restriction site profiling arrays (TRSPAs) - is described for the analysis of such fragments. A totally diagnostic internal control DNA is also described which allows both the extent and exact nature of any partial digestion to be unambiguously determined for inter-population perfectly matched duplex depletion or TRSPA restriction.

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